

GGCGGCGGCA GCCTCGGCTA CAGCTTCGGC GGCGAAGGTC AGCGCCGAGC GCAGCGGCA 60
 CCTGAGGCGG TGACCGACCC GAGCGATTTC CTCTTGGATT TGGCTACACA CTTATAGATC 120
 TTCTGCACCTG TTTACAGGCA CAGTTGCTGA TATGTGTCA AG ATG AGT GGG ATG 174
 Met Ser Gly Met 1
 GGA GAA AAT ACC TCT GAC CCC TCC AGG GCA GAG ACA AGA AAG CGC AAG 222
 Gly Glu Asn Thr Ser Asp Pro Ser Arg Ala Glu Thr Arg Lys Arg Lys 20
 5
 GAA TGT CCT GAC CAA CTT GGA CCC AGC CCC AAA AGG AAC ACT GAA AAA 270
 Glu Cys Pro Asp Gln Leu Gly Pro Ser Pro Lys Arg Asn Thr Glu Lys 35
 25
 CGT AAT CGT GAA CAG GAA AAT AAA TAT ATA GAA GAA CTT GCA GAG TTG 318
 Arg Asn Arg Glu Gln Glu Asn Lys Tyr Ile Glu Glu Leu Ala Glu Leu 45
 40
 ATT TTT GCA AAT TTT AAT GAT ATA GAC AAC TTT AAC TTC AAA CCT GAC 366
 Ile Phe Ala Asn Phe Asn Asp Ile Asp Asn Phe Asn Phe Lys Pro Asp 60
 55
 AAA TGT GCA ATC TTA AAA GAA ACT GTG AAG CAA ATT CGT CAG ATC AAA 414
 Lys Cys Ala Ile Leu Lys Glu Thr Val Lys Gln Ile Arg Gln Ile Lys 70
 75
 GAA CAA GAG AAA GCA GCA GCT GCC AAC ATA GAT GAA GTG CAG AAG TCA 462
 Glu Gln Glu Lys Ala Ala Ala Asn Ile Asp Glu Val Gln Lys Ser 90
 85
 95
 100

FIG. 1A

GAT GTA TCC TCT ACA GGG CAG GGT GTC ATC GAC AAG GAT GCG CTG GGG Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ala Leu Gly	510
105	
CCT ATG ATG CTT GAG GCC CTT GAT GGG TTC TTC TTT GTA GTG AAC CTG Pro Met Met Leu Glu Ala Leu Asp Gly Phe Phe Val Val Asn Leu	558
120	
125	
GAA GGC AAC GTT GTG TTT GTG TCA GAG AAT GTG ACA CAG TAT CTA AGG Glu Gly Asn Val Val Phe Val Ser Glu Asn Val Thr Gln Tyr Leu Arg	606
135	
140	
TAT AAC CAA GAA GAG CTG ATG AAC AAA AGT GTA TAT AGC ATC TTG CAT Tyr Asn Gln Glu Glu Leu Met Asn Lys Ser Val Tyr Ser Ile Leu His	654
150	
155	
GTT GGG GAC CAC ACG GAA TTT GTC AAA AAC CTG CCA AAG TCT ATA Val Gly Asp His Thr Glu Phe Val Lys Asn Leu Pro Lys Ser Ile	702
165	
170	
GTA AAT GGG GGA TCT TGG TCT GGC GAA CCT CGG AGG CGG AAC AGC CAT Val Asn Gly Gly Ser Trp Ser Gly Glu Pro Pro Arg Arg Asn Ser His	750
185	
190	
ACC TTC AAT TGT CGG ATG CTG GTA AAA CCT TTA CCT GAT TCA GAA GAG Thr Phe Asn Cys Arg Met Leu Val Lys Pro Leu Pro Asp Ser Glu Glu	798
200	
205	
GAG GGT CAT GAT AAC CAG GAA GCT CAT CAG AAA TAT GAA ACT ATG CAG Glu Gly His Asp Asn Gln Glu Ala His Gln Lys Tyr Glu Thr Met Gln	846
215	
220	
225	

FIG.1B

TGC TTC GCT GTC TCT CAA AAG TCC ATC AAA GAA GAA GGA GAA GAT Cys Phe Ala Val Ser Gln Pro Lys Ser Ile Lys Glu Gly Gln Asp	894
235	
TTG CAG TCC TGC TTG ATT TGC GTG GCA AGA GTT CCC ATG AAG GAA Leu Gln Ser Cys Leu Ile Cys Val Ala Arg Arg Val Pro Met Lys Glu	942
245	
255	
AGA CCA GTT CTT CCC TCA TCA GAA AGT TTT ACT ACT CGC CAG GAT CTC Arg Pro Val Leu Leu Pro Ser Ser Glu Ser Phe Thr Thr Arg Gln Asp Leu	990
265	
270	
CAA GGC AAG ATC ACG TCT CTG GAT ACC AGC ACC ATG AGA GCA GCC ATG Gln Gly Lys Ile Thr Ser Ser Leu Asp Thr Ser Thr Met Arg Ala Ala Met	1038
280	
285	
AAA CCA GGC TGG GAG GAC CTG GTA AGA AGG TGT ATT CAG AAG TTC CAT Lys Pro Gly Trp Glu Asp Leu Val Arg Arg Cys Ile Gln Lys Phe His	1086
295	
300	
305	
GCG CAG CAT GAA GGA GAA TCT GTG TCC TAT GCT AAG AGG CAT CAT CAT Ala Gln His Glu Gly Glu Ser Val Ser Tyr Ala Lys Arg His His His	1134
310	
315	
GAA GTA CTG AGA CAA GGA TTG GCA TTC AGT CAA ATC TAT CGT TTT TCC Glu Val Leu Arg Gln Gly Leu Ala Phe Ser Gln Ile Tyr Arg Phe Ser	1182
325	
330	
335	
TTG TCT GAT GGC ACT CTT GTT GCT GCA CAA ACG AAG AGC AAA CTC ATC Leu Ser Asp Gly Thr Leu Val Ala Ala Gln Thr Lys Ser Lys Leu Ile	1230
345	
350	
355	

FIG. 1C

CGT TCT CAG ACT ACT AAT GAA CCT CAA CTT GTA ATA TCT TTA CAT ATG Arg Ser Gln Thr Thr Asn Glu Pro Gln Leu Val Ile Ser Leu His Met 360 365 370	1278
CTT CAC AGA GAG CAG AAT GTG TGT ATG AAT CCG GAT CTG ACT GGA Leu His Arg Glu Gln Asn Val Cys Val Met Asn Pro Asp Leu Thr Gly 375 380 385	1326
CAA AGC ATG GGG AAG CCA CTG AAT CCA ATT AGC TCT AAC AGC CCT GCC Gln Thr Met Gly Lys Pro Leu Asn Pro Ile Ser Ser Asn Ser Pro Ala 390 395 400	1374
CAT CAG GCC CTG TGC AGT GGG AAC CCA GGT CAG GAC ATG ACC CTC AGT His Gln Ala Leu Cys Ser Gly Asn Pro Gly Gln Asp Met Thr Leu Ser 405 410 415 420	1422
AGC AAT ATA AAT TTT CCC ATA AAT GGC CCA AAG GAA CAA ATG GGC ATG Ser Asn Ile Asn Phe Pro Ile Asn Gly Pro Lys Glu Gln Met Gly Met 425 430 435	1470
CCC ATG GGC AGG TTT GGT GGT TCT GGG GGA ATG AAC CAT GTG TCA GGC Pro Met Gly Arg Phe Gly Gly Ser Gly Gly Met Asn His Val Ser Gly 440 445 450	1518
ATG CAA GCA ACC ACT CCT CAG GGT AGT AAC TAT GCA CTC AAA ATG AAC Met Gln Ala Thr Thr Pro Gln Gly Ser Asn Tyr Ala Leu Lys Met Asn 455 460 465	1566
AGC CCC TCA CAA AGC AGC CCT GGC ATG AAT CCA GGA CAG CCC ACC TCC Ser Pro Ser Gln Ser Ser Pro Gly Met Asn Pro Gly Gln Pro Thr Ser 470 475 480	1614

FIG.1D

ATG CTT TCA CCA AGG CAT GCG ATG AGC CCT GGA GTG GCT GGC AGC GCT Met Leu Ser Pro Arg His Arg Met Ser Pro Gly Val Ala Gly Ser 485 490 495 500	1662
CGA ATC CCA CCC AGT CAG TTT TCC CCT GCA GGA AGC TTG CAT TCC CCT Arg Ile Pro Pro Ser Gln Phe Ser Pro Ala Gly Ser Leu His Ser Pro 505 510 515	1710
GTG GGA GTT TGC AGC AGC ACA GGA AAT AGC CAT AGT TAT ACC AAC AGC Val Gly Val Cys Ser Ser Thr Gly Asn Ser His Ser Tyr Thr Asn Ser 520 525 530	1758
TCC CTC AAT GCA CTT CAG GCC CTC AGC GAG GGG CAC GGG GTC TCA TTA Ser Leu Asn Ala Leu Gln Ala Leu Ser Glu Gly His Gly Val Ser Leu 535 540 545	1806
GGG TCA TCG TTG GCT TCA CCA GAC CTA AAA ATG GGC AAT TTG CAA AAC Gly Ser Ser Leu Ala Ser Pro Asp Leu Lys Met Gly Asn Leu Gln Asn 550 555 560	1854
TCC CCA GTT AAT ATG AAT CCT CCC CCA CTC AGC AAG ATG GGA AGC TTG Ser Pro Val Asn Met Asn Pro Pro Pro Leu Ser Lys Met Gly Ser 565 570 575 580	1902
GAC TCA AAA GAC TGT TTT GGA CTA TAT GGG GAG CCC TCT GAA GGT ACA Asp Ser Lys Asp Cys Phe Gly Leu Tyr Gly Glu Pro Ser Glu Gly Thr 585 590 595	1950
ACT GGA CAA GCA GAG AGC AGC TGC CAT CCT GGA GAG CAA AAG GAA ACA Thr Gly Gln Ala Glu Ser Ser Cys His Pro Gly Glu Gln Lys Glu Thr 600 605 610	1998

FIG.1E

AAT GAC CCC AAC CTG CCC CGG GCC GTG AGC AGT GAG AGA GCT GAC GGG Asn Asp Pro Asn Leu Pro Pro Ala Val Ser Ser Glu Arg Ala Asp Gly 615	2046
CAG AGC AGA CTG CAT GAC AGC AAA GGG CAG ACC AAA CTC CTG CAG CTG Gln Ser Arg Leu His Asp Ser Lys Gly Gln Thr Lys Leu Leu Gln Leu 630	2094
CTG ACC ACC AAA TCT GAT CAG ATG GAG CCC TCG CCC TTA GCC AGC TCT Leu Thr Thr Lys Ser Asp Gln Met Glu Pro Ser Pro Leu Ala Ser 645	2142
TTG TCG GAT ACA AAC AAA GAC TCC ACA GGT AGC TTG CCT GGT TCT GGG Leu Ser Asp Thr Asn Lys Asp Ser Thr Gly Ser Leu Pro Gly Ser Gly 665	2190
TCT ACA CAT GGA ACC TCG CTC AAG GAG AAG CAT AAA ATT TTG CAC AGA Ser Thr His Gly Thr Ser Leu Lys Glu Lys His Lys Ile Leu His Arg 680	2238
CTC TTG CAG GAC AGC AGT TCC CCT GTG GAC TTG GCC AAG TTA ACA GCA Leu Leu Asp Ser Ser Pro Val Asp Leu Ala Lys Leu Thr Ala 695	2286
GAA GCC ACA GGC AAA GAC CTG AGC CAG GAG TCC AGC AGC ACA GCT CCT Glu Ala Thr Gly Lys Asp Leu Ser Gln Glu Ser Ser Thr Ala Pro 710	2334
GGA TCA GAA GTG ACT ATT AAA CAA GAG CCG GTG AGC CCC AAG AAG AAA Gly Ser Glu Val Thr Ile Lys Gln Glu Pro Val Ser Pro Lys Lys 725	2382

FIG.1F

GAG AAT GCA CTA CTT CGC TAT TTG CTA GAT AAA GAT ACT AAA GAT Glu Asn Ala Leu Leu Arg Tyr Leu Leu Asp Lys Asp Thr 755	2430
ATT GGT TTA CCA GAA ATA ACC CCC AAA CTT GAG AGA CTG GAC AGT AAG Ile Gly Leu Pro Glu Ile Thr Pro Lys Leu Glu Arg Leu Asp Ser Lys 770	2478
ACA GAT CCT GCC AGT AAC ACA AAA TTA ATA GCA ATG AAA ACT GAG AAG Thr Asp Pro Ala Ser Asn Thr Lys Leu Ile Ala Met Lys Thr Glu Lys 785	2526
GAG GAG ATG AGC TTT GAG CCT GGT GAC CAG CCT GGC AGT GAG CTG GAC Glu Glu Met Ser Phe Glu Pro Gly Asp Glu Pro Gly Ser Glu Leu Asp 800	2574
AAC TTG GAG GAG ATT TTG GAT GAT TTG CAG AAT AGT CAA TTA CCA CAG Asn Leu Glu Glu Ile Leu Asp Asp Leu Glu Asn Ser Glu Leu Pro Glu 820	2622
CTT TTC CCA GAC ACG AGG CCA GGC CCT GCT GGA TCA GTT GAC AAG Leu Phe Pro Asp Thr Arg Pro Gly Ala Pro Ala Gly Ser Val Asp Lys 835	2670
CAA GCC ATC ATC AAT GAC CTC ATG CAA CTC ACA GCT GAA AAC AGC CCT Gln Ala Ile Ile Asn Asp Leu Met Gln Leu Thr Ala Glu Asn Ser Pro 850	2718
GTC ACA CCT GTT GGA GCC CAG AAA ACA GCA CTG CGA ATT TCA CAG AGC Val Thr Pro Val Gly Ala Gln Lys Thr Ala Leu Arg Ile Ser Gln Ser 865	2766

FIG.1G

ACT TTT AAT AAC CCA CGA GGG CAA CTG GGC AGG TTA TTG CCA AAC Thr Phe Asn Asn Pro Arg Pro Gly Gln Leu Arg Leu Leu Pro Asn 870 880	2814
CAG AAT TTA CCA CTT GAC ATC ACA TTG CAA AGC CCA ACT GGT GCT GGA Gln Asn Leu Pro Leu Asp Ile Thr Leu Gln Ser Pro Thr Gly Ala Gly 885 890 895 900	2862
CCT TTC CCA CCA ATC AGA AAC AGT AGT CCC TAC TCA GTG ATA CCT CAG Pro Phe Pro Pro Ile Arg Asn Ser Ser Tyr Ser Val Ile Pro Gln 905 910 915	2910
CCA GGA ATG ATG GGT AAT CAA GGG ATG ATA GGA AAC CAA GGA AAT TTA Pro Gly Met Met Gly Asn Gln Gly Met Ile Gly Asn Gln Gly Asn Leu 920 925 930	2958
GGG AAC AGT AGC ACA GGA ATG ATT GGT AAC AGT GCT TCT CGG CCT ACT Gly Asn Ser Ser Thr Gly Met Ile Gly Asn Ser Ala Ser Arg Pro Thr 935 940 945	3006
ATG CCA TCT GGA GAA TGG GCA CCG CAG AGT TCG GCT GTG AGA GTC ACC Met Pro Ser Gly Glu Trp Ala Pro Gln Ser Ser Ala Val Arg Val Thr 950 955 960	3054
TGT GCT GCT ACC ACC AGT GCC ATG AAC CGG CCA GTC CAA GGA GGT ATG Cys Ala Ala Thr Thr Ser Ala Met Asn Arg Pro Val Gln Gly Gly Met 965 970 975 980	3102
ATT CGG AAC CCA GCA GCC AGC ATC CCC ATG AGG CCC AGC AGC CAG CCT Ile Arg Asn Pro Ala Ala Ser Ile Pro Met Arg Pro Ser Ser Gln Pro 985 990 995	3150

FIG.1H

GGC CAA AGA CAG ACG CTT CAG TCT CAG GTC ATG AAT ATA GGG CCA TCT Gly Gln Arg Gln Thr Leu Gln Ser Gln Val Met Asn Ile Gly Pro Ser 1000 1005 1010	3198
GAA TTA GAG ATG AAC ATG GGG GGA CCT CAG TAT AGC CAA CAA GCT Glu Leu Glu Met Asn Met Gly Gly Pro Gln Tyr Ser Gln Gln Gln Ala 1015 1020 1025	3246
CCT CCA AAT CAG ACT GCC CCA TGG CCT GAA AGC ATC CTG CCT ATA GAC Pro Pro Asn Gln Thr Ala Pro Trp Pro Glu Ser Ile Leu Pro Ile Asp 1030 1035 1040	3294
CAG GCG TCT TTT GCC AGC CAA AAC AGG CAG CCA TTT GGC AGT TCT CCA Gln Ala Ser Phe Ala Ser Gln Asn Arg Gln Pro Phe Gly Ser Ser Pro 1045 1050 1055 1060	3342
GAT GAC TTG CTA TGT CCA CAT CCT GCA GCT GAG TCT CCG AGT GAT GAG Asp Asp Leu Leu Cys Pro His Pro Ala Ala Glu Ser Pro Ser Asp Glu 1065 1070 1075	3390
GGA GCT CTC CTG GAC CAG CTG TAT CTG GCC TTG CCG AAT TTT GAT GGC Gly Ala Leu Leu Asp Gln Leu Tyr Leu Ala Leu Arg Asn Phe Asp Gly 1080 1085 1090	3438
CTG GAG GAG ATT GAT AGA GCC TTA GGA ATA CCC GAA CTG GTC AGC CAG Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Ser Gln 1095 1100 1105	3486
AGC CAA GCA GTA GAT CCA GAA CAG TTC TCA AGT CAG GAT TCC AAC ATC Ser Gln Ala Val Asp Pro Gln Gln Phe Ser Ser Gln Asp Ser Asn Ile 1110 1115 1120	3534

FIG. 11

ATG CTG GAG CAG AAG GCG CCC GTT TTC CCA CAG CAG TAT GCA TCT CAG Met Leu Glu Gln Lys Ala Pro Val Phe Pro Gln Gln Tyr Ala Ser Gln 1125 1130 1135	3582
GCA CAA ATG GCC CAG GGT AGC TAT TCT CCC ATG CAA GAT CCA AAC TTT Ala Gln Met Ala Gln Gly Ser Tyr Ser Pro Met Gln Asp Pro Asn Phe 1145 1150 1155	3630
CAC ACC ATG GGA CAG CAG CGG CCT AGT TAT GCC ACA CTC CGT ATG CAG CCC His Thr Met Gly Gln Arg Pro Ser Tyr Ala Thr Leu Arg Met Gln Pro 1160 1165 1170	3678
AGA CCG GGC CTC AGG CCC AGC GGC CTA GTG CAG AAC CAG CCA AAT CAA Arg Pro Gly Leu Arg Pro Thr Gly Leu Val Gln Asn Gln Pro Asn Gln 1175 1180 1185	3726
CTA AGA CTT CAA CTT CAG CAT CGC CTC CAA GCA CAG CAG AAT CGC CAG Leu Arg Leu Gln Leu Gln His Arg Leu Gln Ala Gln Gln Asn Arg Gln 1190 1195 1200	3774
CCA CTT ATG AAT CAA ATC AGC AAT GTT TCC AAT GTG AAC TTG ACT CTG Pro Leu Met Asn Gln Ile Ser Asn Val Ser Asn Val Asn Leu Thr Leu 1205 1210 1215	3822
AGG CCT GGA GTA CCA ACA CAG GCA CCT ATT AAT GCA CAG ATG CTG GCC Arg Pro Gly Val Pro Thr Gln Ala Pro Ile Asn Ala Gln Met Leu Ala 1220 1225 1230 1235	3870
CAG AGA CAG AGG GAA ATC CTG AAC CAG CAT CTT CGA CAG AGA CAA ATG Gln Arg Gln Arg Glu Ile Leu Asn Gln His Leu Arg Gln Arg Gln Met 1240 1245 1250	3918

FIG.1J

CAT CAG CAA CAG CAA GTT CAG CAA CGA ACT TTG ATG ATG AGA GGA CAA His Gln Gln Gln Val Gln Gln Arg Thr Leu Met Met Arg Gly Gln 1255 1260 1265	3966
GGG TTG AAT ATG ACA CCA AGC ATG GTG GCT CCT AGT GGT ATG CCA GCA Gly Leu Asn Met Thr Pro Ser Met Val Ala Pro Ser Gly Met Pro Ala 1270 1275 1280	4014
ACT ATG AGC AAC CCT CGG ATT CCC CAG GCA AAT GCA CAG CAG TTT CCA Thr Met Ser Asn Pro Arg Ile Pro Gln Ala Asn Ala Gln Gln Phe Pro 1285 1290 1295 1300	4062
TTT CCT CCA AAC TAC GGA ATA AGT CAG CAA CCT GAT CCA GGC TTT ACT Phe Pro Pro Asn Tyr Gly Ile Ser Gln Gln Pro Asp Pro Gly Phe Thr 1305 1310 1315	4110
GGG GCT ACG ACT CCC CAG AGC CCA CTT ATG TCA CCC CCA ATG GCA CAT Gly Ala Thr Thr Pro Gln Ser Pro Leu Met Ser Pro Arg Met Ala His 1320 1325 1330	4158
ACA CAG AGT CCC ATG ATG CAA CAG TCT CAG GCC AAC CCA GCC TAT CAG Thr Gln Ser Pro Met Met Gln Gln Ser Gln Ala Asn Pro Ala Tyr Gln 1335 1340 1345	4206
GCC CCC TCC GAC ATA AAT GGA TGG GCG CAG GGG AAC ATG GGC GGA AAC Ala Pro Ser Asp Ile Asn Gly Trp Ala Gln Gly Asn Met Gly Gly Asn 1350 1355 1360	4254
AGC ATG TTT TCC CAG CAG TCC CCA CCA CAC TTT GGG CAG CAA GCA AAC Ser Met Phe Ser Gln Gln Ser Pro Pro His Phe Gly Gln Gln Ala Asn 1365 1370 1375	4302

FIG.1K

ACC AGC ATG TAC AGT AAC ATG AAC ATC AAT GTG TCC ATG GCG ACC Thr Ser Met Tyr Ser Asn Asn Met Asn Ile Asn Val Ser Met Ala Thr 1385 1390 1395	4350
AAC ACA GGT GGC ATG AGC AGC ATG AAC CAG ATG ACA GGA CAG ATC AGC Asn Thr Gly Gly Met Ser Ser Met Asn Gln Met Thr Gly Gln Ile Ser 1400 1405 1410	4398
ATG ACC TCA GTG ACC TCC GTG TCT AGG TCA GGG CTG TCC TCC ATG GGT Met Thr Ser Val Thr Ser Val Ser Thr Ser Gly Leu Ser Ser Met Gly 1415 1420 1425	4446
CCC GAG CAG GTT AAT GAT CCT GCT CTG AGG GGA GGC AAC CTG TTC CCA Pro Glu Gln Val Asn Asp Pro Ala Leu Arg Gly Gly Asn Leu Phe Pro 1430 1435 1440	4494
AAC CAG CTG CCT GGA ATG GAT ATT AAG CAG GAG GGA GAC ACA ACA Asn Gln Leu Pro Gly Met Asp Met Ile Lys Gln Glu Gly Asp Thr Thr 1445 1450 1455	4542
CGG AAA TAT TGC TGACACTGCT GAAGCCAGTT GCCTCTTCAG CTGACCGGGC Arg Lys Tyr Cys	4594
TCACCTTGCTC AAAACACTTC CAGTCTGGAG AGCTGTGTCT ATTGTGTTCA ACCCAACTGA	4654
CCTGCCAGCC GGTTCTGCTA GAGCAGACAG GCCTGGCCCT GGTTCCCAGG GTGGCGTCCA	4714
CTGGGCTGTG GCAGGAGGAG CTGCCTCTTC TCTTGACAGT CTGAAGCTCG CATCCAGACA	4774
GTGCGTCACT CTGTTCCCTG CATTCACCTT AGTGCAACTT AGATCTCTCC TCCCAAGTA	4834

FIG.1L

AATGTTGACA GGCCAATTC ATACCATGT CAGATTGAAT GTATTTAAAT GTATGTATTT 4894
 AGGAGAACC ATGCTCTGT TCTGTTCTG TTGGTTCCA GACACTGGTT TCTTGCTTTG 4954
 TTTTCCTGG CTAAACAGTCT AGTGCAAAAG ATTAAGATTT TATCTGGGG AAAGAAAAGA 5014
 ATTTTTAAA AAATTAACCT AAAGATGTTT TAAGCTAAAG CCTGAATTTG GGATGGAAGC 5074
 AGGACAGACA CCGTGGACAG CGCTGTATTT ACAGACACAC CCAGTGGGTG AAGACCAACA 5134
 AAGTCACAGT CGTATCTCTA GAAAGCTCTA AAGACCATGT TGGAAAGAGT CTCAGTTAC 5194
 TGAACAGATG AAAAGGAGCC TGTGAGAGGG CTGTTAACAT TAGCAAATAT TTTTTCCTTG 5254
 TTTTTCTTT GTTAAACCA AACTGGTTCA CCTGAATCAT GAATTGAGAA GAAATAATTT 5314
 TCATTTCCTAA ATTAAGTCCC TTTAGTTTG ATCAGACAGC TTGAATCAGC ATCTCTCTTT 5374
 CCCTGTGAGC CTGACTCTTC CCTCCCTC TCTATTCC CATACTCCCT ATTTTCATTC 5434
 CTTTTTAAA AAATAATATA AGCTACAGAA ACCAGGTAAG CCCTTTATTT CCTTAAATGT 5494
 TTTGCCAGCC ACTTACCAAT TGCTAAGTAT TGAATTTGAG AAAAAAAA TGCATTTACT 5554
 GGCAAGGAGA AGAGCAAGT TAAGGCTTGA TACCAATCGA GCTAAGGATA CCTGCTTTGG 5614
 AAGCATGTTT ATTCGTGTTCC CAGCAACTC TGGCCTCCAA AATGGGAGAA ACGCCAGTGT 5674
 GTTTAAATTG ATAGCAGATA TCAGCAGAGA TTTAACTCT GCCATGTTT TTTTATTTTG 5734
 TTTTTTAGCA GTGCTGACTA AGCGAAGTT TTGTAAGGTA CATAAAAATCC AATTATATG 5794

FIG. 1M

TAAACAAGCA ATAATTTAAG TTGAGAACTT ATGTGTTTTA ATGTATAAT TTTTGTGAGG 5854
 TATACATATT GTGGMAATTGA CTCAAAAATG AGGTACTTCA GTATTAAATT AGATATCTTC 5914
 ATAGCAATGT CTCTAAAGG TGTTTTGTAA AGGATATCAA TGCCTTGATT AGACCTAATT 5974
 TGTAGACTTA AGACTTTTTA TTTTCTAAAC CTTGTGATTC TGCCTATAAG TCAITTTATCT 6034
 AATCTATATG ATATGCAGCC GCTGTAGGAA CCAATTCTTG ATTTTATAT GTTTATATTC 6094
 TTTCCTTAATG AACCTTAGAA AGACTACATG TTAATAAGCA GGCACATTTT ATGGTTGTTT 6154
 TT 6156

FIG.1N

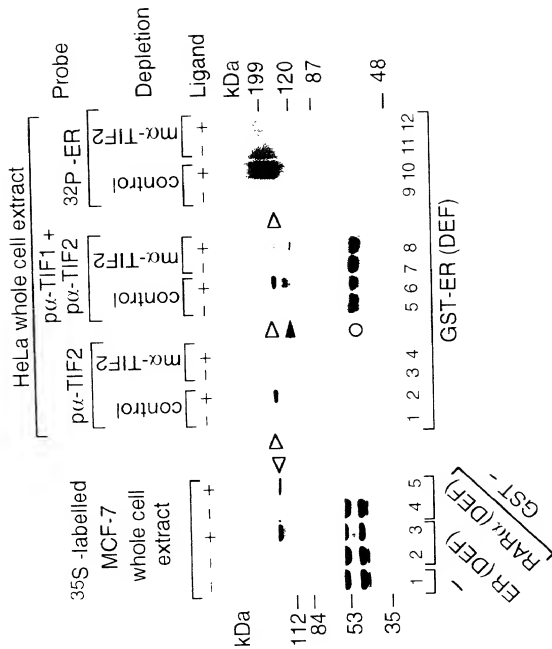


FIG.2B

FIG.2A

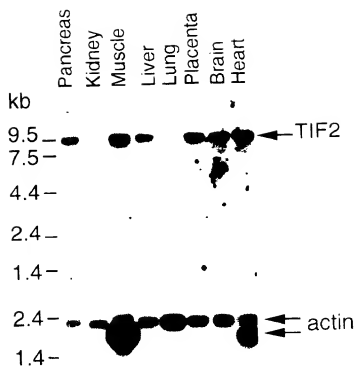


FIG.2C

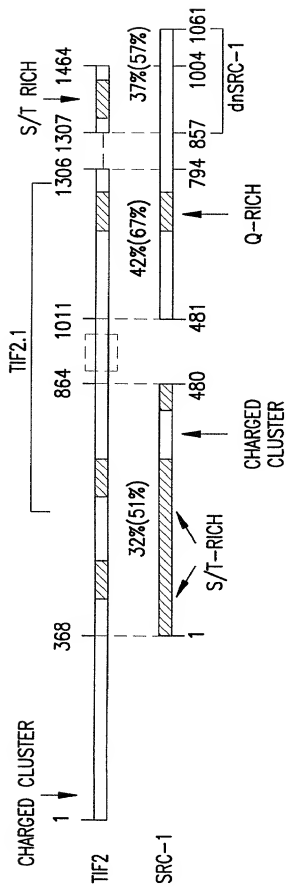
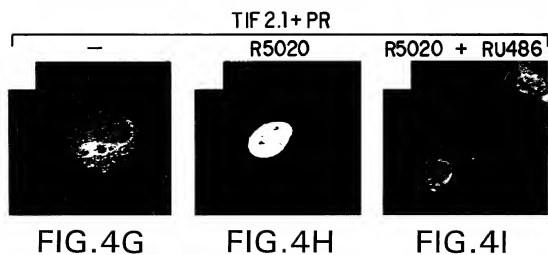
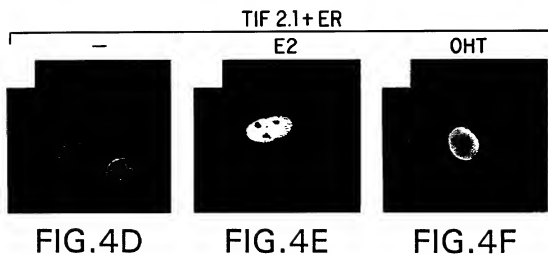
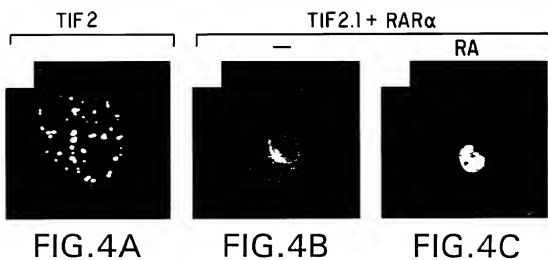


FIG.3C



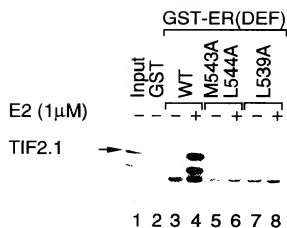


FIG.4K

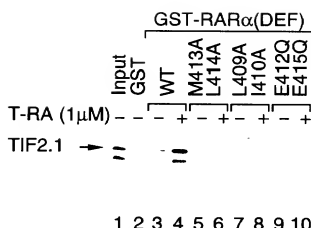


FIG.4L

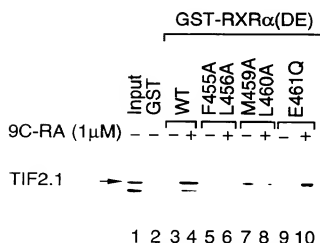


FIG.4M

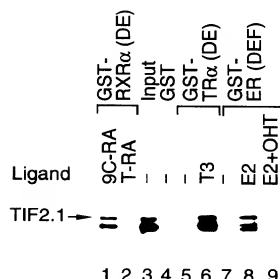


FIG.4N

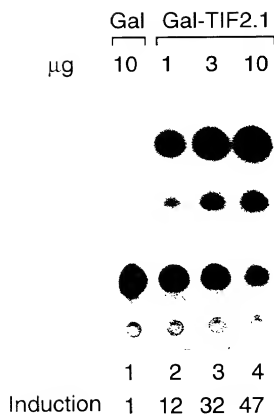


FIG.5A

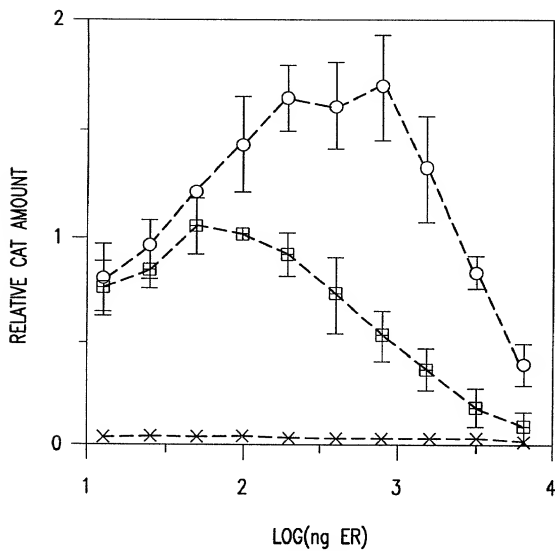


FIG.5B

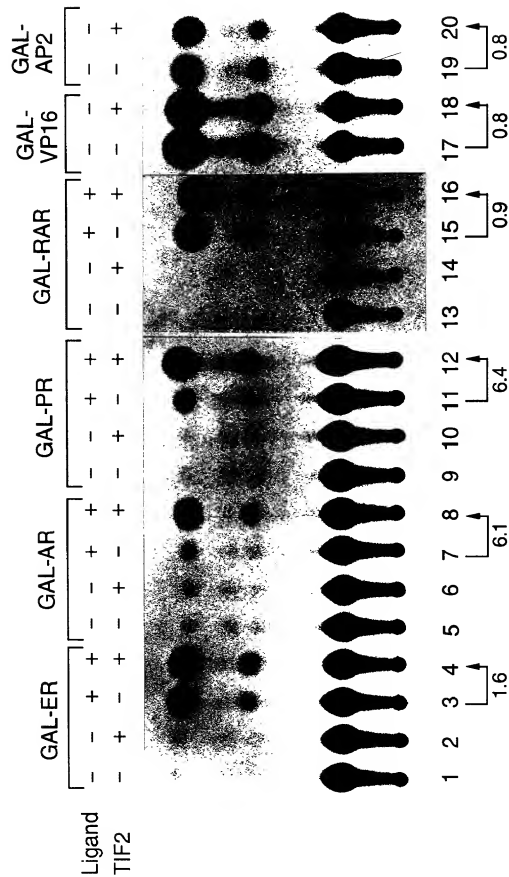


FIG.5C

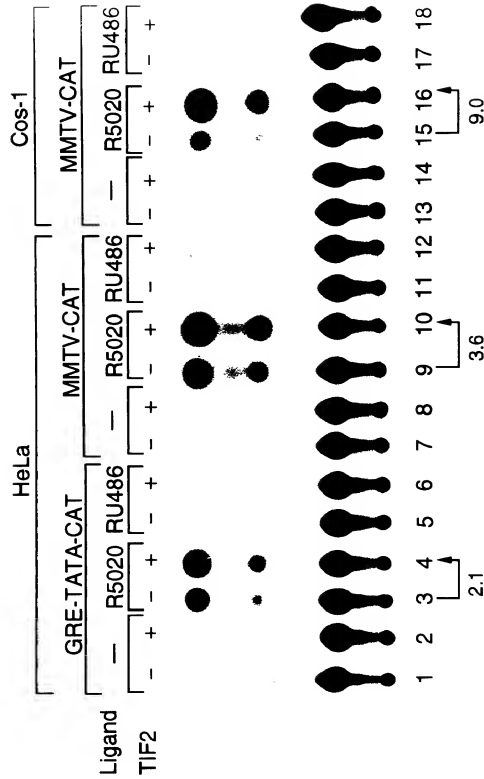


FIG.5D

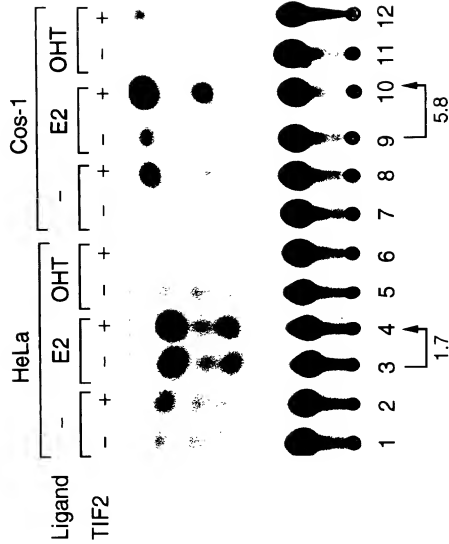


FIG. 5E

RECEPTORS

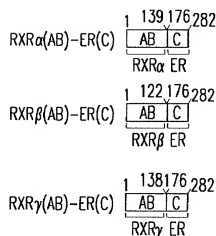
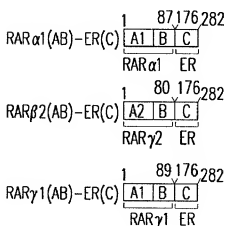
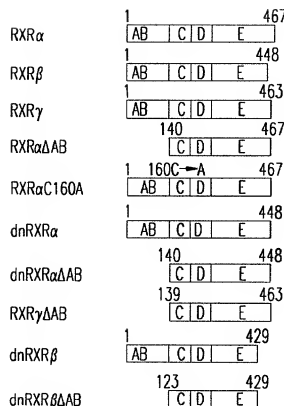
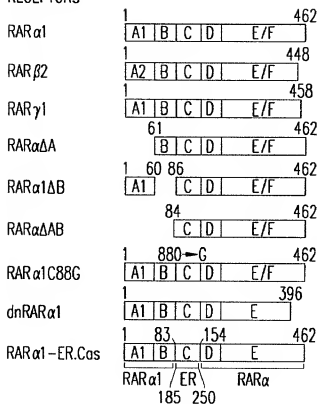


FIG.6B

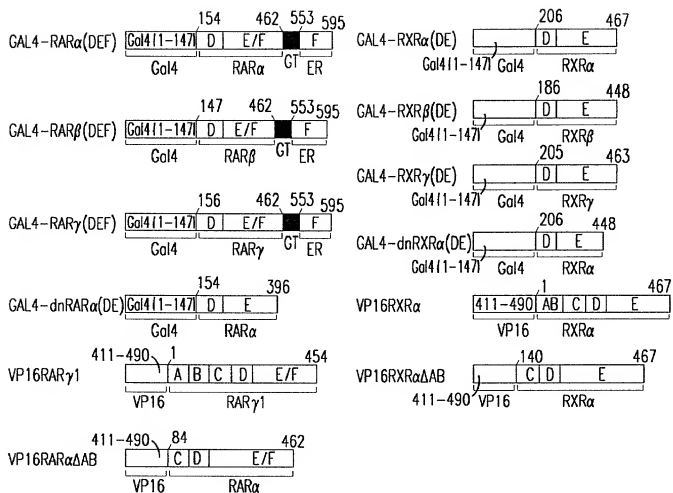


FIG.6C

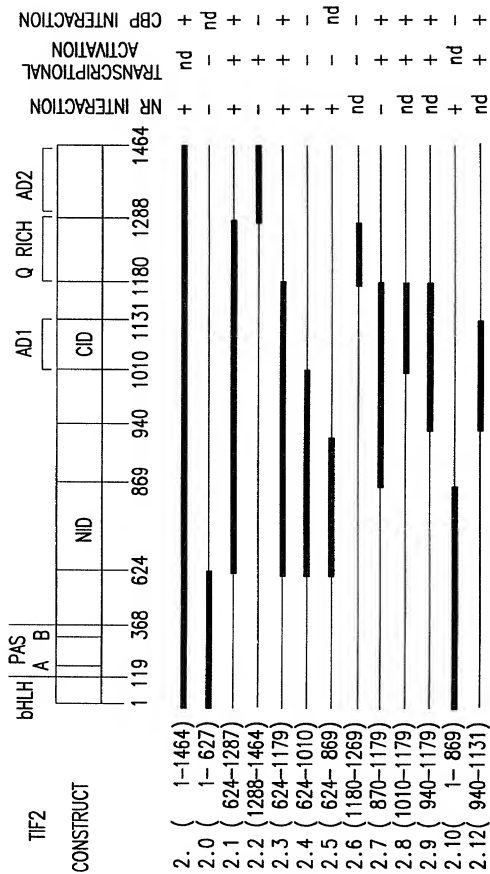


FIG.7A

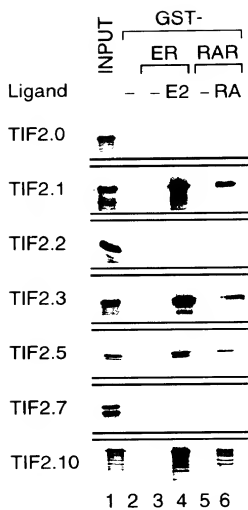


FIG.7B



FIG.7D












WB Cos-1	GAL- TIF	Fold Induction of (17M)5-G-CAT	
		Cos-1	HeLa
	2.0	< 2	< 2
	2.1	32 ± 9	14 ± 2
	2.2	60 ± 5	31 ± 5
	2.3	172 ± 16	122 ± 19
	2.4	< 2	< 2
	2.5	< 2	< 2
	2.6	< 2	< 2
	2.8	324 ± 16	1220 ± 28
	2.7	300 ± 74	1002 ± 67
	2.9	298 ± 19	610 ± 31
	2.12	592 ± 29	772 ± 16

FIG.7C

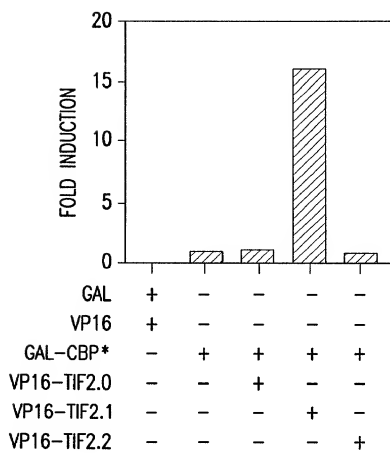


FIG.7E

NR box

TIF1 α	724	-	RS	LT	S	L	L	N	S	-	735
RIP140	933	-	F	N	V	L	K	Q	L	L	SEN - 944
TRIP3	95	-	S	A	T	L	R	S	L	L	NPH - 106
TIF2(I)	638	-	Q	T	K	L	L	Q	L	L	TTKS - 648
TIF2(II)	687	-	H	K	I	L	H	R	L	L	QDSS - 698
TIF2(III)	742	-	N	A	L	L	R	Y	L	L	DKDD - 753

FIG.8B

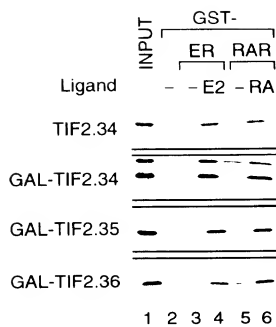


FIG.8C

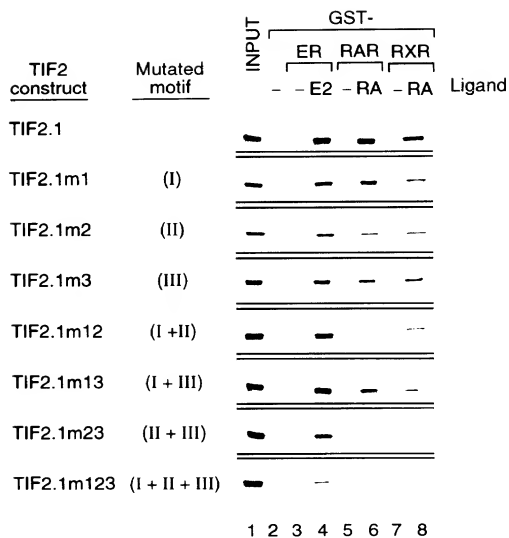


FIG.8D

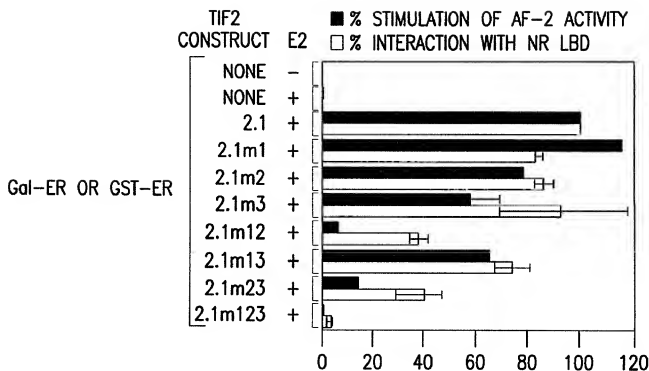


FIG.8E

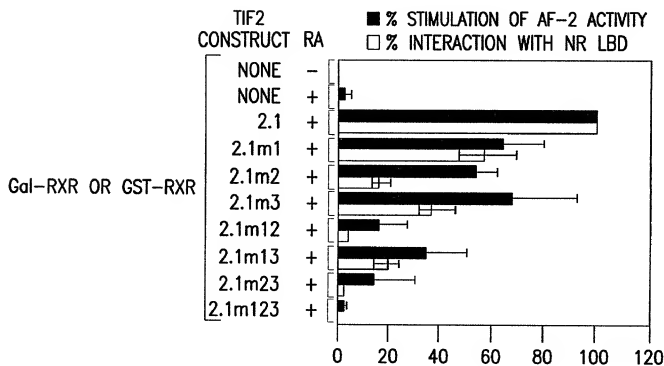


FIG.8F

SRC-1	909-1SSQLDELLCPPTVEGRNDEKALLEQLVSFISGKQETELAEIDRALGIDKLVOGGILD-967	TRANSCRIPTIONAL ACTIVITY	CBP INTERACTION
TIF2	1056-FCSSPDILLCPHPAAE SPSDECALLDQLYLAL...RNF DGL EE IDRALGIPELV SSSQA-1111	++	++
p/CIP	1037-LRNSLDLLGPPSNAGGGSIERALLDQLHTFISNTDGTGL EE IDRALGIPELV NGQA-1094	++	++
TIF2.13	1011P	++	++
TIF2.13(LL)	1011P	++	++
TIF2.13(QQ)	1011P	++	++
TIF2.14	1011P	++	++
TIF2.15	1011P	++	++
TIF2.16	1021P	++	++
TIF2.17	1031N	++	++
TIF2.18	1041L	++	++
TIF2.19	1011P	++	++
TIF2.20	1011P	++	++
TIF2.21	1041L	++	++
TIF2.24	1011P	++	++
TIF2.27	1041L	++	++
TIF2.29	1011P	++	++
TIF2.30	1011P	++	++
TIF2.31	1011P	++	++
TIF2.32	1011P	++	++
TIF2.32(LL)	1011P	++	++
TIF2.32(QQ)	1011P	++	++

FIG.9A

Fold Induction of
(17m)5-TATA-CAT

GAL-TIF	[
	<u>Cos-1</u>	<u>HeLa</u>
2.13	462 ± 9	704 ± 33
2.14	392 ± 13	674 ± 23
2.15	279 ± 21	316 ± 49
2.16	390 ± 34	597 ± 54
2.17	389 ± 50	581 ± 58
2.18	314 ± 16	432 ± 19
2.19	341 ± 67	777 ± 30
2.20	107 ± 11	314 ± 27
2.21	129 ± 8	173 ± 22
2.24	< 2	< 2
2.27	< 2	< 2
2.29	< 2	< 2
2.30	98 ± 13	117 ± 6
2.31	35 ± 3	34 ± 3
2.32	2.8 ± 0.2	5.9 ± 0.9
2.32(LL)	1.4 ± 0.2	1.5 ± 0.1
2.32(DQ)	1.7 ± 0.3	1.2 ± 0.2

FIG.9B

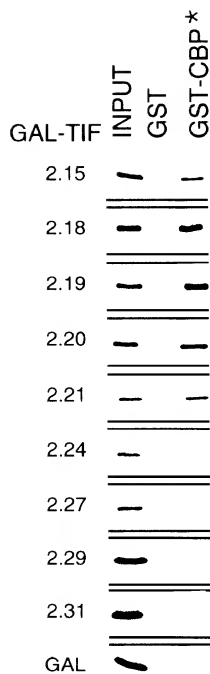


FIG.9C

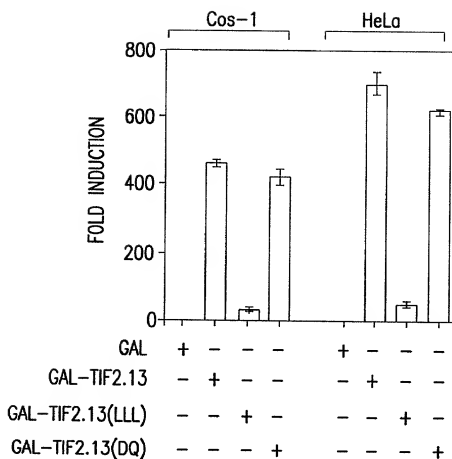


FIG.10A

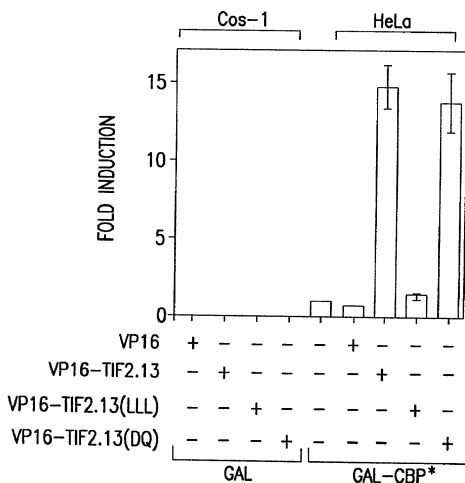


FIG.10B

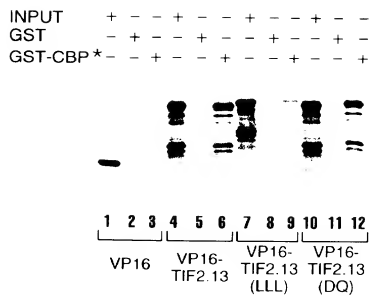


FIG.10C

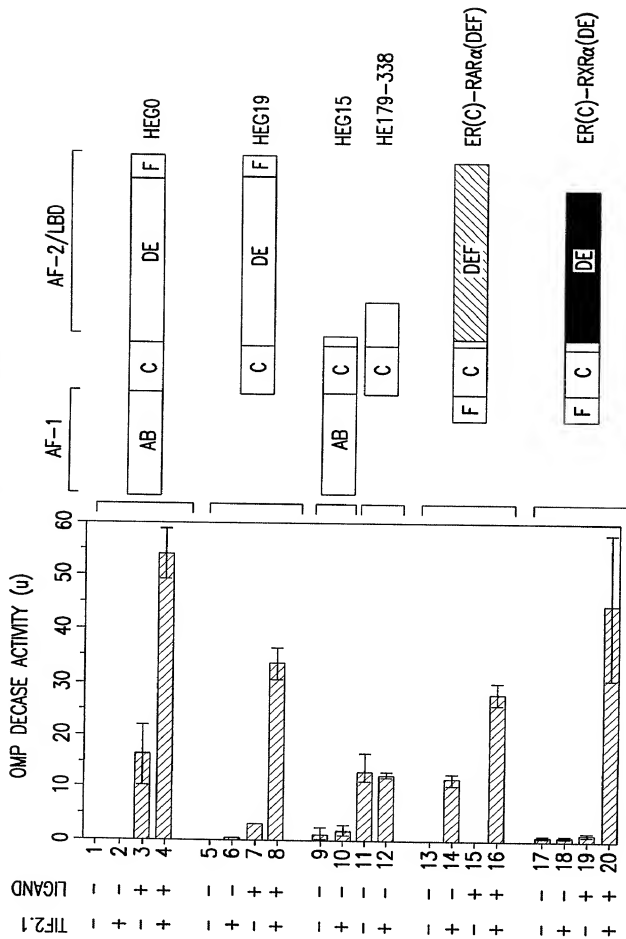


FIG.11

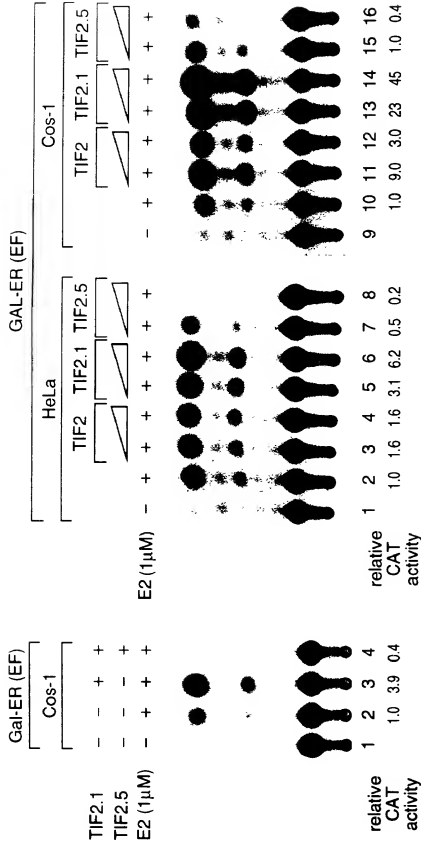


FIG.12A

FIG.12B

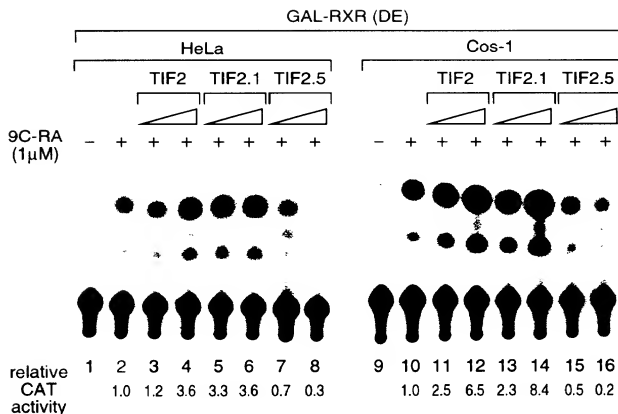


FIG.12C

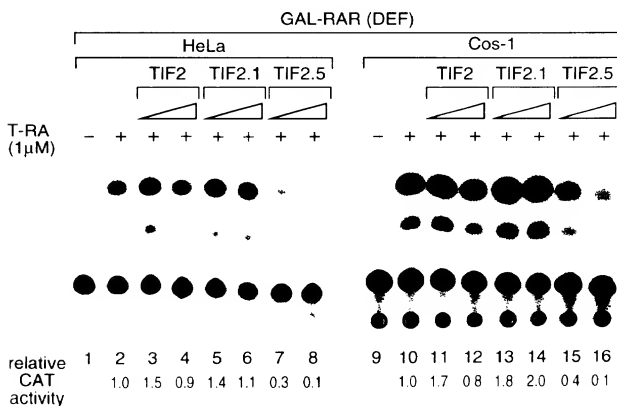


FIG.12D